CLAIMS

1. Nucleotide sequence of cyanophage S-2L, characterized in that it corresponds to SEQ ID No. 1.

2. Nucleotide sequence of cyanophage S-2L, characterized in that it is chosen from:
   a) a nucleotide sequence comprising at least 80% identity with SEQ ID No. 1;
   b) a nucleotide sequence hybridizing under high stringency conditions with SEQ ID No. 1;
   c) a nucleotide sequence which complements SEQ ID No. 1 or which complements a nucleotide sequence as defined in a), or b), or a nucleotide sequence of the corresponding RNA;
   d) a nucleotide sequence of a representative fragment of SEQ ID No. 1, or of a representative fragment of a nucleotide sequence as defined in a), b) or c);
   e) a nucleotide sequence comprising a sequence as defined in a), b), c) or d); and
   f) a nucleotide sequence modified from a nucleotide sequence as defined in a), b), c), d) or e).

3. Nucleotide sequence according to claim 2, characterized in that it codes for a polypeptide chosen from:
   a) the polypeptides of cyanophage S-2L of sequences SEQ ID No. 2 to SEQ ID No. 527;
   b) preferably the polypeptides of sequence SEQ ID No. 14, 18, 26, 68, 86, 92, 105, 109, 134, 142, 143, 148, 152, 169, 175, 187, 208, 211, 234, 246, 250, 257, 264, 286, 298, 316, 332, 342, 347, 348, 351, 355, 364, 365, 369, 370, 392, 395, 406, 418, 422, 425, 429, 432, 433, 454, 464, 466, 472, 484, 489, 494, 500;
   c) preferably also the polypeptides of sequence SEQ ID No. 86, 92, 152, 175, 234, 257, 298, 316, 395, 406, 425, 484;
   d) the polypeptides having at least 80% preferably 85%, 90%, 95% and 98% identity with a polypeptide from a), b), c);
   e) the biologically active fragments of the polypeptides from a), b), c), d)
   f) the polypeptides modified from a), b), c), d), e).

4. Nucleotide sequence characterized in that it comprises a nucleotide sequence chosen from:

a) a nucleotide sequence according to claim 3;
b) a nucleotide sequence comprising at least 80% identity with a nucleotide sequence according to claim 3;
c) a nucleotide sequence hybridizing under high stringency conditions with a nucleotide sequence according to claim 3;
d) a complementary or RNA nucleotide sequence corresponding to a sequence as defined in a), b) or c);
e) a nucleotide sequence fragment representative of a sequence as defined in a), b), c) or d); and
f) a nucleotide sequence modified from a sequence as defined in a), b), c), d) or e).

5. Polypeptide encoded by a nucleotide sequence according to one of claims 2 to 4.

6. Polypeptide according to claim 5, characterized in that it is chosen from the peptides of sequence SEQ ID No. 2 to 527, preferably from the sequences SEQ ID No. 14, 18, 26, 68, 86, 92, 105, 109, 134, 142, 143, 148, 152, 169, 175, 187, 208, 211, 234, 246, 250, 257, 264, 286, 298, 316, 332, 342, 347, 348, 351, 355, 364, 365, 369, 370, 392, 395, 406, 418, 422, 425, 429, 432, 433, 454, 464, 466, 472, 484, 489, 494, 500;

7. Polypeptide according to claim 5 or 6, characterized in that it is chosen from the sequences SEQ ID No. 86, 92, 152, 175, 234, 257, 298, 316, 395, 406, 425, 484;

8. Polypeptide characterized in that it comprises a polypeptide chosen from:
a) a polypeptide according to one of claims 5 to 7;
b) a polypeptide having at least 80% identity with a polypeptide according to one of claims 5 to 7;
c) a fragment of at least 5 amino acids of a polypeptide according to one of claims 5 to 7, or as defined in b);

d) a biologically active fragment of a polypeptide according to one of claims 5 to 7, or as defined in b) or c); and

e) a polypeptide modified from a polypeptide according to one of claims 5 to 7, or as defined in b), c) or d).

9. Nucleotide sequence according to one of claims 2 to 4, characterized in that it codes for a polypeptide of cyanophage S-2L, involved in the biosynthesis of nucleotides, purines, pyrimidines or nucleosides or for one of its representative fragments.

10. Nucleotide sequence according to one of claims 2 to 4, characterized in that it codes for a polypeptide of cyanophage S-2L, involved in the biosynthesis of D-bases or for one of its representative fragments.

11. Nucleotide sequence according to claim 10, characterized in that it codes for a peptide of sequence SEQ ID No. 175.

12. Nucleotide sequence according to one of claims 2 to 4, characterized in that it codes for a polypeptide of cyanophage S-2L, involved in the replication process, or for one of its representative fragments, preferably a peptide of sequence SEQ ID No. 14, 18, 142, 355, 429, 454 (DNA polymerase, topoisomerase activity).

13. Nucleotide sequence according to one of claims 2 to 4, characterized in that it codes for a polypeptide of cyanophage S-2L, involved in the transcription process, or for one of its representative fragments, preferably a peptide of sequence SEQ ID No. 92, 143, 187, 234, also preferably SEQ ID No. 92.

14. Nucleotide sequence according to one of claims 2 to 4, characterized in that it codes for an envelope polypeptide of cyanophage S-2L, or one of its representative fragments, preferably a peptide of sequence SEQ ID No. 169, 316, 351, 392, 395, 406, 422, 425, in particular a peptide of sequence SEQ ID No. 395, 406, 425.

15. Nucleotide sequence according to one of claims 2 to 4, characterized in that it codes for a polypeptide of cyanophage S-2L involved in the rerouting of the cell machinery or one of its representative fragments.

16. Nucleotide sequence according to one of claims 2 to 4, characterized in that it codes for a polypeptide of cyanophage S-2L involved in virulence or one of its representative fragments, preferably a peptide of sequence SEQ ID No. 257.

17. Polypeptide according to one of claims 5 to 8, characterized in that it is a polypeptide of cyanophage S-2L involved in the biosynthesis of nucleotides, purines, pyrimidines or nucleosides.

18. Polypeptide according to one of claims 5 to 8, characterized in that it is a polypeptide of cyanophage S-2L involved in the biosynthesis of D-bases, preferably a peptide of sequence SEQ ID No. 175 or a representative fragment.

19. Polypeptide according to one of claims 5 to 8, characterized in that it is a polypeptide of cyanophage S-2L involved in the replication process, preferably a peptide of sequence SEQ ID No. 14, 18, 142, 355, 429, 454 or a representative fragment.

20. Polypeptide according to one of claims 5 to 8, characterized in that it is a polypeptide of cyanophage S-2L, involved in the transcription process, preferably a peptide of sequence SEQ ID No. 92, 143, 187 or a representative fragment.

21. Polypeptide according to one of claims 5 to 8, characterized in that it is an envelope polypeptide of cyanophage S-2L, preferably a peptide of sequence SEQ ID No. 169, 316, 351, 392, 395, 406, 422, 425 or a representative fragment.

22. Polypeptide according to one of claims 5 to 8, characterized in that it is a polypeptide of cyanophage S-2L involved in intermediate metabolism, or a representative fragment.

23. Polypeptide according to one of claims 5 to 8, characterized in that it is a polypeptide of cyanophage S-2L involved in the process of rerouting the cell machinery or one of its fragments.

24. DNA chip or filter, characterized in that it contains at least one nucleotide sequence according to any one of claims 2 to 4.

25. Cloning and/or expression vector, characterized in that it contains a nucleotide sequence according to one of claims 3 or 4 or 9 to 16.

26. Cloning and/or expression vector according to claim 25, characterized in that it contains a nucleotide sequence according to claim 10 or 11, in particular coding for a protein involved in the sythesis of D-bases.

27. Cloning and/or expression vector according to claim 25, characterized in that it contains a nucleotide sequence according to claim 11 or 12, in particular coding for a polymerase capable of polymerizing D-bases.

28. Host cell, characterized in that it is transformed by a vector according to one of claims 25 to 27.

29. Host cell according to claim 28, characterized in that it is a bacterium.

30. Process for preparing a polypeptide of interest, characterized in that a cell transformed by a vector according to one of claims 25 to 27 is cultured under conditions allowing the expression of said polypeptide, and in that said recombinant polypeptide is recovered.

31. Process according to claim 30, characterized in that the polypeptide of interest is a protein involved in the metabolism of D-bases, in particular succinyladenylate synthetase.

32. Process according to claim, characterized in that the polypeptide of interest is a polymerase of cyanophages S-2L, capable of polymerizing D-bases.

33. Recombinant polypeptide capable of being obtained by a process according to claim 30.

34. Monoclonal or polyclonal antibody, its fragments, or chimeric antibody, characterized in that it is capable of specifically recognizing a polypeptide according to one of claims 5 to 8 or 17 to 23.

35. Antibody according to claim 34, characterized in that it is a marked antibody.

36. Protein chip characterized in that it contains at least one polypeptide according to one of claims 5 to 8 or 17 to 23, or at least one antibody according to one of claims 34 or 35, immobilized on the support of said chip.

37. Process for detection and/or identification of cyanophage S-2L or of a related phage in a biological sample, characterized in that it uses a nucleotide sequence according to one of claims 3 to 4 or 9 to 16.

38. Process for obtaining D-bases and/or polynucleotides of interest comprising at least one D-base, comprising the culture of a microorganism containing at least one nucleotide sequence of cyanophage S-2L coding for at least one polypeptide involved in the synthesis of D-bases, under appropriate conditions for the development of the vector and the synthesis of D-bases and/or said polynucleotides of interest.

39. Process according to claim 38 comprising:
    - the addition to a medium comprising the substrates required for obtaining D-bases, of an extract or mixture of extracts of recombinant bacteria expressing at least one gene of cyanophage S-2L involved in the synthesis of D-bases
    - if appropriate the extraction of the polynucleotides of interest.

40. Process according to claim 38 comprising:

- the preparation of at least one DNA sequence coding for a polypeptide capable of provoking the synthesis of at least one D-base in a host microorganism
- the cloning of said coding sequence in a vector capable of being transferred into and replicating in said host microorganism, this vector comprising the elements necessary for the expression of said coding sequence
- the transfer of the vector comprising said coding sequence into a microorganism capable of producing the enzymes of the D-base synthesis directed by said coding sequence
- the culture of the microorganism under appropriate conditions for the development of the vector and the synthesis of the D-bases
- if appropriate the extraction of D-bases and/or of said polynucleotides of interest.

41. Process for obtaining D-bases and/or polynucleotides of interest comprising at least one D-base, said process comprising:
    - the addition, to a medium comprising the substrates required for obtaining D-bases, of the expression product of at least one gene of cyanophage S-2L involved in the synthesis of D-bases, in order to produce D-bases and/or polynucleotides of interest comprising at least one D-base
    - the extraction of the D-bases and/or said polynucleotides of interest.

42. Process for obtaining polynucleotides of interest comprising at least one D-base, said process comprising the culture of a microorganism containing at least one nucleotide sequence of cyanophage S-2L coding for at least one polypeptide involved in the extension of said polynucleotides with incorporation of D-bases, DNA polymerase in particular, in appropriate conditions for the development of the vector and the extension of said polynucleotides.

43. Process according to any one of claims 38 to 42 characterized in that the gene involved in the synthesis of the D-bases is the gene of succinyladenylate synthetase.

44. Process according to any one of claims 38 to 42 characterized in that it comprises a stage of amplification, in the presence of cyanophage D polymerase and appropriate primers, of polynucleotides comprising at least one D-base.

45. Process for selection of compounds capable of stimulating or inhibiting the synthesis of D-bases and/or polynucleotides of interest incorporating at least one D-base, comprising the addition to the synthesis medium of the tested compound and comparison of the synthesis in the presence and in the absence of said compound.

46. Use of cyanophage S-2L for obtaining DNA polymerase or RNA polymerase involved in the metabolism of the D-bases.

47. Use of cyanophage S-2L for the production of nucleotides of interest not obtained naturally comprising at least one D-base, dDMP and dDTP.

48. Strain of cyanophage S-2L deposited at the CNCM No. I-2619 characterized in that it contains at least one nucleotide sequence according to claims 1 to 4.

49. Process for producing a gene bank of cyanophage S-2L characterized in that the process comprises the following stages:
    a) Culture of purified cyanophages S-2L from the species *Synechococcus*,
    b) Fragmentation of the DNA extracted by the sonication technique,
    c) Cloning of the Shotgun bank obtained in an *E. coli* vector, and
    d) Sequencing of the clones until the genome is completely covered.

50. Gene bank of cyanophage S-2L deposited on 24th January 2001 at the C.N.C.M. according to the provisions of the Budapest Treaty, and registered under accession number 1-2619 obtained by a process according to claim 49.

51. Plasmids contained in recombinant bacteria deposited at the C.N.C.M. under reference number 1-2619.

52. Recombinant bacteria such as deposited at the C.N.C.M. under reference number 1-2619.